

FIGURE 1

Clone LR4: hLH/CG Receptor Fusion with Thioredoxin Gene in pET32 Vector

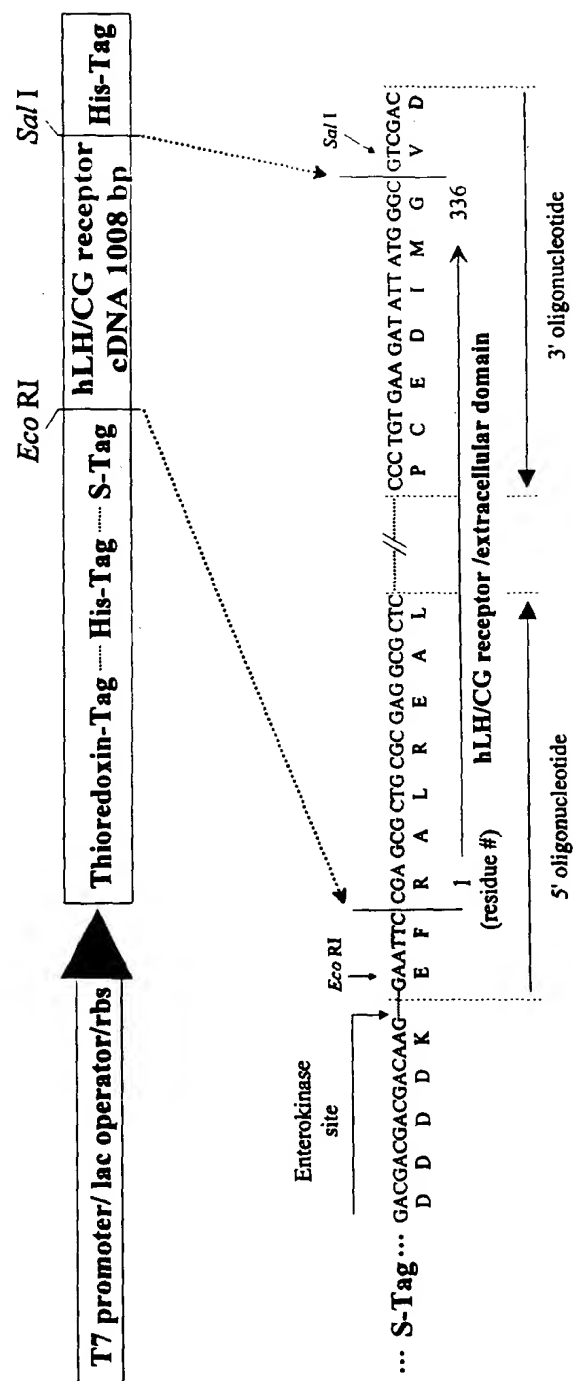
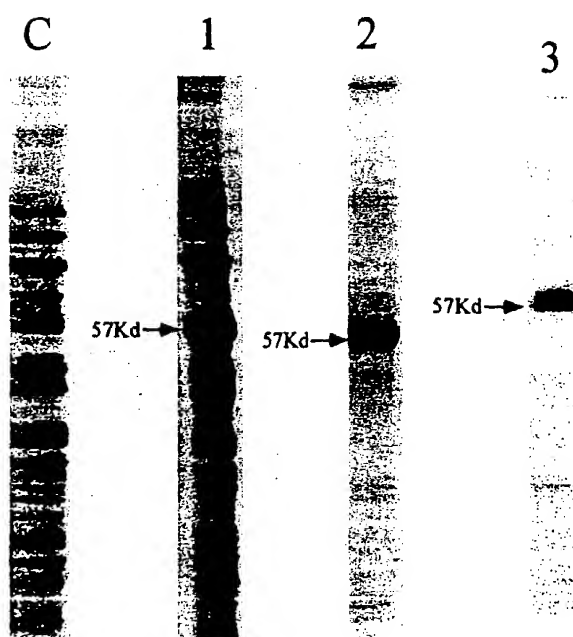


FIGURE 2

Non-reducing protein gels

Panel A



Western blots

Panel B

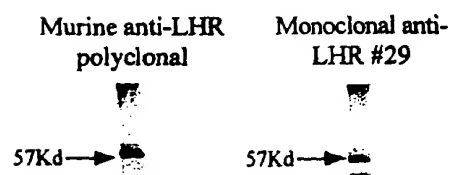


FIGURE 3

Affinity of hLH/CG receptor fusion protein

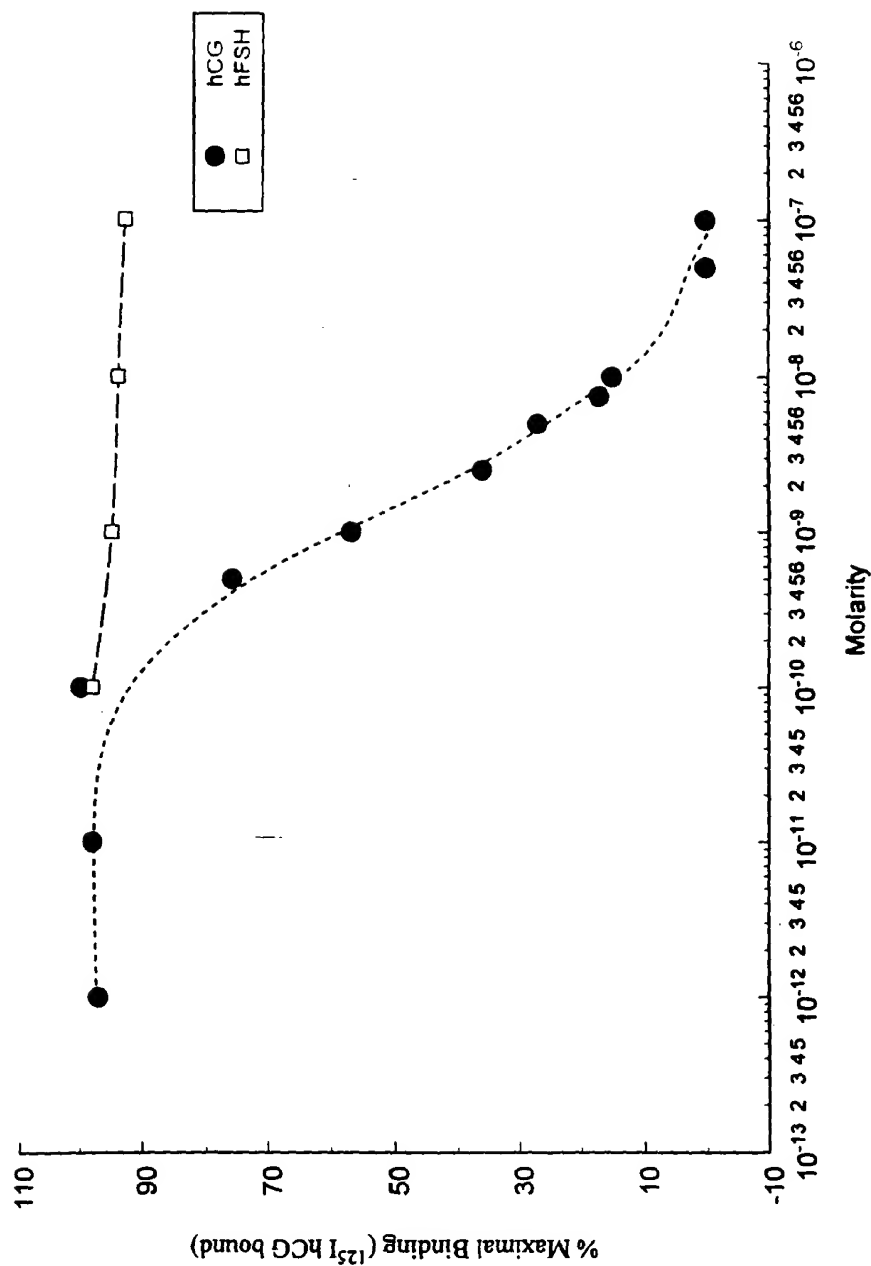


FIGURE 4

Effect of anti-hCG monoclonal antibodies
on hCG binding to receptor fusion protein

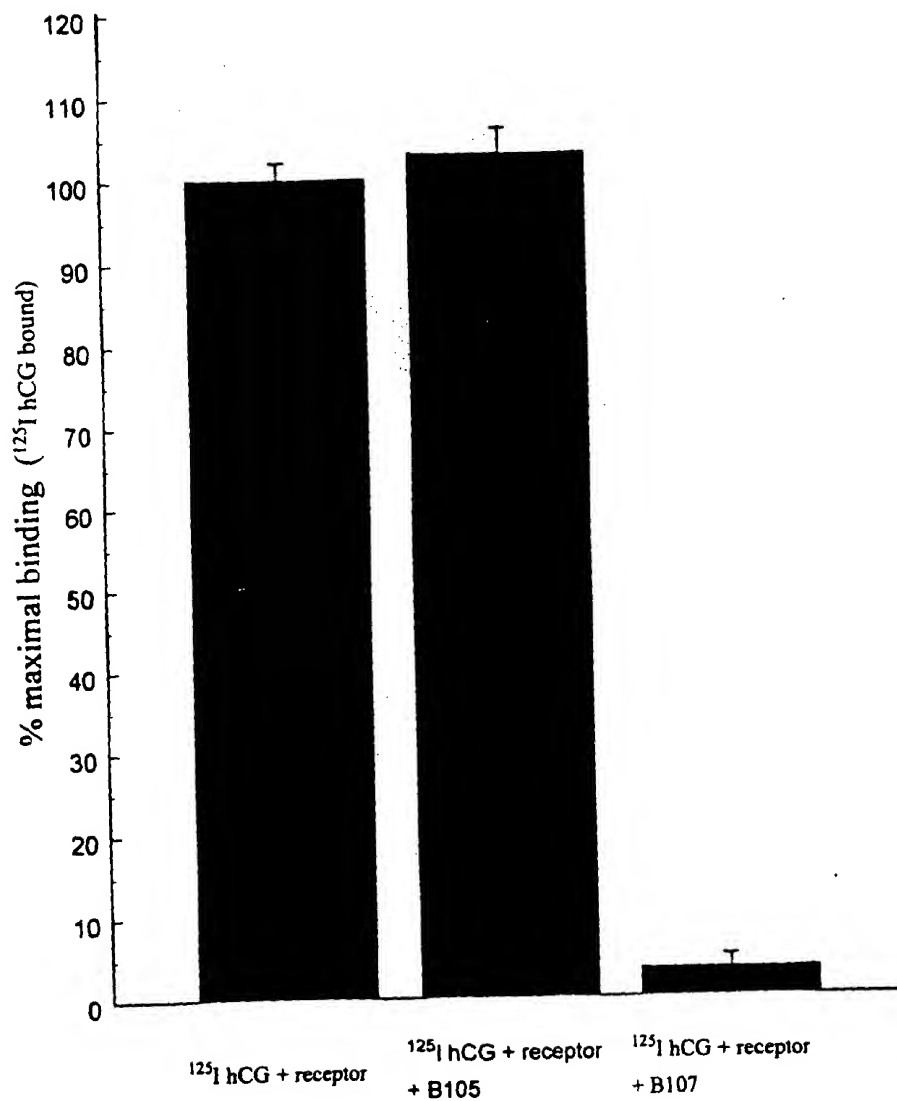
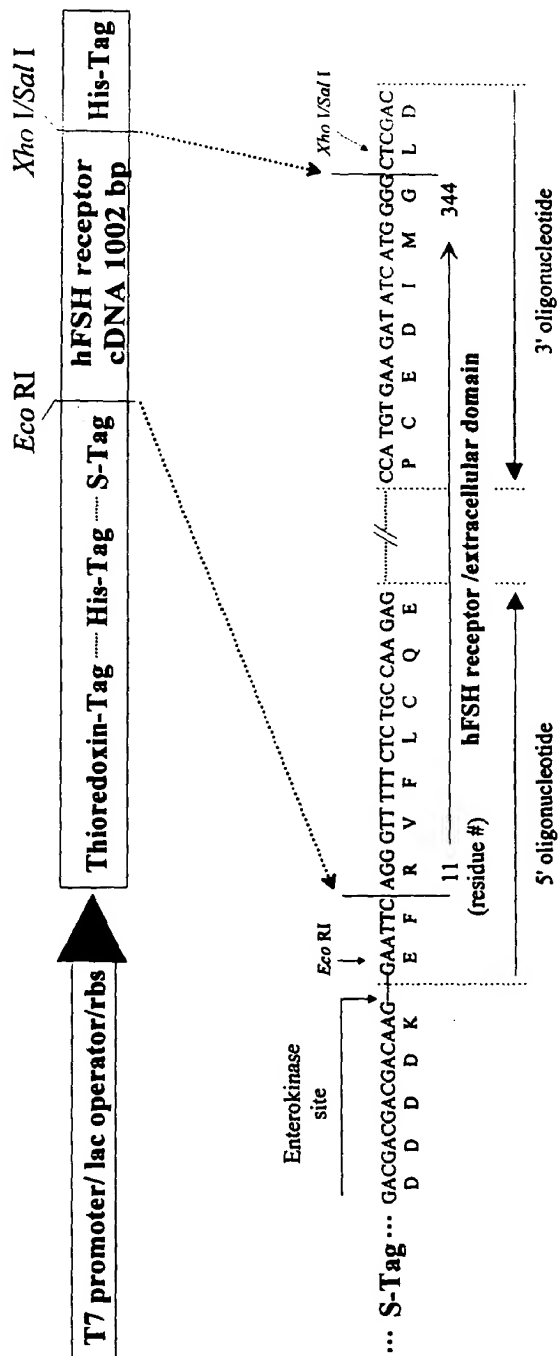


FIGURE 5

hFSH Receptor Fusion with Thioredoxin Gene in pET32 Vector



1 atgagcgataaaattattcacctgactgac
31 gacagttttgacacggatgcttactcaaagcg
61 gacggggcgatcctcgctgatttctgggca
91 gagtgggtgcgggtccgtgcaaaatgatcgcc
121 ccgattctg gatgaaatcgctgacgaatat
151 cagggcaaaactgaccgttgcaaaactgaac
181 atcgatcaaaaccctggcactgcgccgaaa
211 tatggcatccgtgggtatcccgaactctgctg
241 ctgttcaaaaacgggtgaagtggcgggcaacc
271 aaagtgggtgcaactgtctaaaggtcagttg
301 aaagagttcctcgacgctcaaacctggcgggt
331 tctggttctggccatatgcaccatcatcat
361 catcattcttcttggtctggtgccacgcggt
391 tctggtatgaaagaaaccgctgctgctaaa
421 ttcgaacgccagcacatggacagcccagat
451 ctgggtaccgacgacgacgacaaggccatg
481 gctgatatcggatccgaattcaggggtttt
511 ctctgccaaagagagcaagggtgacagagt
541 ccttctgacctcccagggaattgccattgaa
571 ctgaggtttgtcctcaccaaagcttcgagtc
601 atccaaaaaggtgcaatttccaggatttggg
631 gacctggagaaaaatagagatctctcagaat
661 gatgtcttggagggtgatagaggcagatgtg
691 ttctccaaccttcccaaattacatgaaatt
721 agaattgaaaaggccaacaacctgctctac
751 atcacccctgaggccttccagaaccttccc
781 aaccttcaatatctgttaatatccaacaca
811 ggtattaagcaccttcagatgttcacaag
841 attcattctctccaaaagggtttacttgac
871 attcaagataacataaaacatccacacaatt
901 gaaagaaattcttctggtggggtgagcttt
931 gaaagtgtgattctatggctgaataagaat
961 gggattcaagaaatacacaactgtgcattc
991 aatggaacccaactagatgcagtgaattcta
1021 agcgataataataatttagaagaattgct
1051 aatgatgttttccacggagcctctggacca
1081 gtcattctagatatattcaagacaaggatc
1111 cattccctgctgctatgggttagaaaat
1141 cttaaagaagctgagggccagggtcgacttac
1171 aacttaaaaaagctgcctactctggaaaag
1201 cttgtcgccctcatggaagccagcctcacc
1231 tatccagccattgctgtgaccttggcaaac
1261 tggagacggcaaatctctgagcttcatcca
1291 atttgcaacaaatctattttaaggccaagaa
1321 gttgattatatgactcaggctaggggtcag
1351 agatcctctctggcagaagacaatgagtc
1381 agctacagcagagggttgacatgacgtac
1411 actgagtttgactatgacttatgcaatgaa
1441 gtggttgacgtgacctgctcccctaagcca
1471 gatgcattcaaccatgtgaagatatcatg
1501 ggggtcgacaagccttgcggccgcactcgag
1531 caccaccaccaccaccactga

1 MSDKIIHLTDDSFDTDLVKADGAILVDFWA
31 EWC GPC KMIAPILDEIADEYQGKLTVAKLN
61 IDQNP GTAPKYGIRGIPTLLLLFKNGEVAAT
91 KVGALSKGQLKEFLDANLAGSGSGMHMHHH
121 HHSSGLVPRGSGMKETAAAKFERQHMDSPD
151 LGTDDDDKAMADIGSEFRVFLCQESKVTEI
181 PSDLP RNAIELRFVLTKLRVIOKGA FSGFG
211 DLEKIEISQNDVLEIVADVFSNLPKLHEI
241 RIEKANLLYITPEAFQNLPNLQYLLISNT
271 GIKHLPDVHKIHS LQKVLLDIQDNINIHTI
301 ERNSFVGLSFESVILWLNKNGIQEIHNCAF
331 NGTQLDAVNLS DNNNLEELPNDV FHGASGP
361 VILDISRTRIHSLPSYGLENLKKLRARSTY
391 NLKKLP TLEKLVALMEASLTYP SHCCAFAN
421 WRRQISELHPICNKSILRQEV DYM TQARGQ
451 RSSLAEDNESSY SRGFDMTYTEFDYDLCNE
481 VVDVTCSPKPD AFNPCEDIMGVDKLAAALE
511 HHHHHH*

Figure 7A

1 atgagcgataaaattattcacctgactgac
 31 gacagttttgacacggatgtactcaaagcg
 61 gacggggcgatcctcgtcgatttctgggca
 91 gagtgggtgcgggtccgtgcaaaatgatcgcc
 121 ccgattctggatgaaatcgctgacgaatat
 151 caggggcaaaactgaccgttgcaaaactgaac
 181 atcgatcaaaaccctggcactgcgcccgaac
 211 tatggcatccgtgggtatcccgaactctgctg
 241 ctgttcaaaaacgggtgaagtggcgggcaacc
 271 aaagtgggtgcactgtctaaagggtcagttg
 301 aaagagttcctcgacgctaaccctggccggt
 331 tctgggttctggccatatgcacatcatcat
 361 catcattcttctggtctggtgccacgcggt
 391 tctgggtatgaaagaaaccgctgctgctaaa
 421 ttcgaacgccagcacatggacagcccagat
 451 ctgggtaccgacgacgacgacaaggccatg
 481 gctgatatcggtatccgaattccgagcgtg
 511 cgcgaggcgctctgccctgagccctgcaac
 541 tgcgtgcccgcacggcgccctgcgctgccc
 571 ggccccacggcgggtctcactcgactatca
 601 cttgcctacctccctgtcaaagtgatecca
 631 tctcaagctttcagaggacttaatgaggtc
 661 ataaaaattgaaatctctcagattgattcc
 691 ctggaaaggatagaagctaattgcctttgac
 721 aacctcctcaatttctgtgaaatactgatc
 751 cagaacacacaaaaatctgagatacattgag
 781 cccggagcattttataaatcttccccgatta
 811 aaatacttgagcatctgtaacacaggcatc
 841 agaaagtttccagatgttacgaagggtctc
 871 tcctctgaatcaaatttcattctggaaatt
 901 tgtgataacttacacataaccaccatacca
 931 ggaaatgcttttcaagggtgaataatgaa
 961 tctgtaacactcaaaactatatggaaatgga
 991 tttgaagaagtacaaagtcattgcaatt
 1021 gggaacgacactgacttcaactggagctaaag
 1051 gaaaacgtacatctggagaagatgcacaat
 1081 ggagccttccgtggggccacagggccgaaa
 1111 accttggtatatttcttccaccaaattgcag
 1141 gccctgcccagctatggccctagagtcatt
 1171 cagaggctaattgccacgtcattctattct
 1201 ctaaaaaaattgccatcaagagaaacattt
 1231 gtcaatctcctggaggccacgttgacttac
 1261 cccagccactgctgtgcttttagaaacttg
 1291 ccaacaaaagaacagaatttttcacattcc
 1321 atttctgaaaacttttccaaacaatgtgaa
 1351 agcacagtaaggaaagtgaataacaaaaca
 1381 ctttattcttccatgcttgctgagagtga
 1411 ctgagtggtgctgggactatgaatatggttc
 1441 tgcttaccacaaagacaccccgatgtgctcct
 1471 gaaccagatgcttttaatccctgtgaagat
 1501 attatgggcgtcgacaagcttgcggccgca
 1531 ctcgagcaccaccaccaccaccactga

Figure 7B

1 MSDKIIHLTDDSFDTDVLKADGAILVDFWA
31 EWCGPCKMIAPILDEIADEYQGKLTVAKLN
61 IDQNPGTAPKYGIRGIPTLLLFKNGEVAAT
91 KVGALSKGQLKEFLDANLAGSGSGHMHMHHH
121 HHSSGLVPRGSGMKETAAAKFERQHMDSPD
151 LGTDDDDDKAMADIGSEFRALREALCPEPCN
181 CVPDGALRCPGPTAGLTRLSLAYLPVKVIP
211 SQAFRGLNEVIKIEISQIDSLERIEANAFD
241 NLLNLSEILIQNTKNLRYIEPGAFINLPRL
271 KYLSICNTGIRKFPDVTKVFSSESFILEI
301 CDN LHITTIPGNAFQGMNNE SVTLKLYGNG
331 FEEVQSHAFNGTTLTSLELKENVHLEKMHN
361 GAFRGATGPKTLDISSTKLQALPSYGLES
391 QRLIATSSSYSLKKLPSRETFVNLEATLTY
421 PSHCCAFRNLP TKEQNFSHSISENFSKQCE
451 STVRKVNNKTLYSSMLAESEL SGWDY EYGF
481 CLPKTPRCAPEPDAFNPCEDIMGVDKLAAA
511 LEHHHHHH*

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